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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/383,551

DATE: 11/10/1999
TIME: 15:51:47

Input Set: I383551.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Tamatani, Takuya
2 Tezuka, Katsunari
3 <120> TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL ADHESION AND SIGNAL
4 <130> FILE REFERENCE: 06501/039001
5 <140> CURRENT APPLICATION NUMBER: US/09/383,551
6 <141> CURRENT FILING DATE: 1999-08-26
7 <150> EARLIER APPLICATION NUMBER: WO PCT/JP98/00831
8 <151> EARLIER FILING DATE: 1998-02-21
9 <150> EARLIER APPLICATION NUMBER: JP 10/62217
10 <151> EARLIER FILING DATE: 1998-02-26
11 <150> EARLIER APPLICATION NUMBER: JP 9/62290
12 <151> EARLIER FILING DATE: 1997-02-27
13 <160> NUMBER OF SEQ ID NOS: 15
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25 1 5 10 15
26 gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata 96
27 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
28 20 25 30
29 ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc 144
30 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
31 35 40 45
32 cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat 192
33 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
34 50 55 60
35 ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg 240
36 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
37 65 70 75 80
38 aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta 288
39 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
40 85 90 95
41 tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca 336
42 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
43 100 105 110
44 att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg 384
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47      cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc      432
48      His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
49              130                      135                      140
50      ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt      480
51      Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
52      145                      150                      155                      160
53      att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct      528
54      Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
55              165                      170                      175
56      aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct      576
57      Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
58              180                      185                      190
59      aga ctc aca gat gtg acc cta taa      600
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70              20                      25                      30
71      Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
72              35                      40                      45
73      Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
74              50                      55                      60
75      Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
76              65                      70                      75                      80
77      Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
78              85                      90                      95
79      Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
80              100                      105                      110
81      Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
82              115                      120                      125
83      His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
84              130                      135                      140
85      Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
86      145                      150                      155                      160
87      Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
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89      Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
90              180                      185                      190
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94      <211> LENGTH: 2610

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100     atttcacaac ggaggtgtac aaattttatg caaatatcct gacattgtcc agcaatttaa      180
101     aatgcagttg ctgaaagggg ggcaaatact ctgcgatctc actaagacaa aaggaagtgg      240
102     aaacacagtg tccattaaga gtctgaaatt ctgccattct cagttatcca acaacagtgt      300
103     ctcttttttt ctatacaact tggaccattc tcatgccaac tattacttct gcaacctatc      360
104     aatttttgat cctcctcctt ttaaagtaac tcttacagga ggatatttgc atatttatga      420
105     atcacaactt tgttgccagc tgaagttctg gttacccata ggatgtgcag cctttgttgt      480
106     agtctgcatt ttgggatgca tacttatttg ttggcttaca aaaaagaagt attcatccag      540
107     tgtgcacgac cctaacggtg aatacatggt catgagagca gtgaacacag ccaaaaaatc      600
108     tagactcaca gatgtgaccc tataatatgg aactctggca ccaggcatg aagcacgttg      660
109     gccagttttc ctcaacttga agtgcaagat tctcttattt ccgggaccac ggagagtctg      720
110     acttaactac atacatcttc tgctggtgtt ttgttcaatc tggaagaatg actgtatcag      780
111     tcaatgggga ttttaacaga ctgccttggt actgccaggt cctctcaaaa caaacacct      840
112     cttgcaacca gctttggaga aagcccagct cctgtgtgct cactgggagt ggaatccctg      900
113     tctccacatc tgctcctagc agtgcacag ccagtaaaac aaacacattt acaagaaaaa      960
114     tgttttaaag atgccagggg tactgaatct gcaaagcaaa tgagcagcca aggaccagca      1020
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118     ttaccaagac tttagatgct ttcttgtgcc ctcaattttc tttttaaaaa tacttctaca      1260
119     tgactgcttg acagcccaac agccactctc aatagagagc tatgtcttac attctttcct      1320
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124     ttcatggtgc tattaattac aagtttagtt cttttttagt atcatattaa aattgcaaac      1620
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128     tgagagactc ccctgagcca gaggccacta ggtattcttg ctcccagagg ctgaagtcac      1860
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130     gtgtcagggc acaattccct ctcataaaaa ccacacagcc tggaaattgg ccctggccct      1980
131     tcaagatagc cttctttaga atatgatttg gctagaaaga ttcttaaata tgtggaatat      2040
132     gattattctt agctggaata ttttctctac ttctgtctg catgccaag gcttctgaag      2100
133     cagccaatgt cgatgcaaca acatttgtaa ctttaggtaa actgggatta tgtttagtt      2160
134     taacattttg taactgtgtg cttatagttt acaagtgaga cccgatatgt cattatgcat      2220
135     acttatatta tcttaagcat gtgtaatgct ggatgtgtac agtacagtac wtaacttgta      2280
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139     aagcatggga cacctcaaga tgaataataa ttcacaaaat ttctgtgaaa tcaaattccag      2520
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143 <211> LENGTH: 2072
144 <212> TYPE: DNA

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152 1 5
153 gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103
154 Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
155 10 15 20
156 gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151
157 Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
158 25 30 35
159 att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
160 Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
161 40 45 50 55
162 ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
163 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
164 60 65 70
165 gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
166 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
167 75 80 85
168 tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
169 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
170 90 95 100
171 ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt 391
172 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
173 105 110 115
174 caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439
175 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
176 120 125 130 135
177 ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487
178 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
179 140 145 150
180 gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
181 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
182 155 160 165
183 aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583
184 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
185 170 175 180
186 atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc 631
187 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr
188 185 190 195
189 tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct 684
190 Ser
191 200
192 gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac 744
193 tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa 804
194 tttcagcaga ctgccctggg tttgctgagt ccttttaagg caaacccctt cttatagaag 864

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196      cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa      984
197      tgccagggtta tgaatctgta aagtacacag gcagccattg accaccgtct gtccctcgttt    1044
198      tttcagattc tatttttttc catagagatc agcattcctt ctagaatcag acagtagagg    1104
199      gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt    1164
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201      cctgcttttg ccttcaagtc tccccttaaa gatactccca caggtctact tgggtggcctg    1284
202      cagccactct gaataggaag tttggtctac aatttccccc ctctgctgct caaaaaaaaaa    1344
203      aattagtaga tatgattttc ccatattctc cctgccaaag taattttttc cagcaaagac    1404
204      atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa catttctcag    1464
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208      ccgaaaactg cagtttctgt ggggtggctgc cagactacag ccgtgctttg ctctggcctt    1704
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211      raattacaga ggggccaaga cagagttccc tcccctagaa actgtgcagc ctggaagtca    1884
212      gccctggcac tttaagatag ccttctttag aacatgagtt agttggtagt attctgacgt    1944
213      gtaaacagcc tatkgttgct cggagctgga ccattttctc cacttccctg tctgcatgcc    2004
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215      aaaaaaaaaa                                2072
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227      ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca      96
228      Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
229      20          25          30
230      ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc      144
231      Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
232      35          40          45
233      cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa      192
234      Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
235      50          55          60
236      ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca      240
237      Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
238      65          70          75          80
239      atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta      288
240      Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
241      85          90          95
242      aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
243      Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
244      100          105          110

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

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